

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 14:59:23 ; Search time 42 seconds
(without alignments)
801.406 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDKALLSLNDFASLSPAE.....LENNIITLSTDRPLQGV 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_76: *
2: PIR1: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	453.5	25.2	278	2 T40916	nggl-interacting f
2	384.5	21.4	288	2 S64243	hypothetical prote
3	285.5	15.9	373	2 A69954	conserved hypotet
4	278	15.5	366	2 F89936	conserved hypotet
5	264	14.7	268	2 G97060	uncharacterized pr
6	263.5	14.6	372	2 D83822	hypothetical prote
7	256	14.2	373	2 AH1618	conserved hypotet
8	240	13.3	373	2 AD1256	conserved hypotet
9	225	12.5	241	2 D81341	hypothetical prote
10	216.5	12.0	379	2 B70777	hypothetical prote
11	209.5	11.6	263	2 A12207	hypothetical prote
12	203.5	11.3	265	2 D95187	conserved hypotet
13	203.5	11.3	265	2 E98054	conserved hypotet
14	199.5	11.1	385	2 T44719	hypothetical prote
15	198	11.0	262	2 G82901	conserved hypotet
16	193	10.7	243	2 F71876	hypothetical prote
17	191	10.6	249	2 G64415	hypothetical prote
18	187.5	10.4	257	2 A86639	hypothetical prote
19	181	10.1	243	2 G64639	conserved hypotet
20	148	8.2	251	2 H90568	conserved hypotet
21	133	7.4	247	2 AC0588	conserved hypotet
22	129	7.2	247	2 E64806	hypotet protein - Esc
23	129	7.2	247	2 G90720	hypothetical prote
24	129	7.2	247	2 E85571	hypothetical prote
25	117	6.5	248	2 C70158	conserved hypotet
26	112	6.2	256	2 C82119	conserved hypotet
27	109.5	6.1	316	2 E41830	RNA-directed DNA p
28	107	5.9	250	2 B71107	hypothetical prote
29	106	5.9	252	2 A83089	conserved hypotet

30	105.5	5.9	566	2 A72329	general secretion
31	102	5.7	249	2 D81954	hypothetical prote
32	100	5.6	249	2 G81011	conserved hypotet
33	98.5	5.5	1199	2 T13946	probable adaptor r
34	98	5.4	1093	2 H84126	cation efflux syst
35	97.5	5.4	245	2 H69471	conserved hypotet
36	97.5	5.4	502	1 SKPSXR	general secretion
37	97	5.4	250	2 D75054	hypothetical prote
38	97	5.4	253	2 B84328	hypothetical prote
39	97	5.4	272	2 C75560	conserved hypotet
40	97	5.4	468	2 B64690	replicative DNA he
41	96.5	5.4	248	2 A10328	conserved hypotet
42	96.5	5.4	279	2 S64007	hypothetical prote
43	96	5.3	486	2 F71825	replicative DNA he
44	95.5	5.3	373	2 D71635	hypothetical prote
45	95	5.3	784	2 H64487	elf-4A family prob

ALIGNMENTS

```
RESULT 1
T40916
nggl-interacting factor 3 homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T40916
R/Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, December 1998
A:Reference number: 221956
A:Accession: T40916
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-278 <MDR>
A:Cross-references: EMBL:AL034490; PIDN:CAA22481.1; GSPDB:GNO0068; SPDB:SPCC126.12
A:Experimental source: strain 972h-; cosmid C126
A:Gene: SPDB:SPCC126.12
A:Map position: 3
A:Introns: 72/1; 177/1; 234/1
C:Superfamily: conserved hypothetical protein YGL144c

Query Match          25.2%; Score 453.5; DB 2; Length 278;
Best Local Similarity 32.7%; Pred. No. 5.5e-29;
Matches 116; Conservative 53; Mismatches 93; Indels 93; Gaps 11;

QY 4 KALLS-----LNDPFLSLFSAESNDVNGLLVE-PSPPHYVNTLFLINDLIEEVEVLOK 57
   ||||| : : : : : ||||| ||| : : : ||||| : : :
Db 3 KANISSKLKKKVEISIVNPKLADSWDNTGLLEAFPRTNASSVLLFTDLEKVAEBAISN 62

QY 58 K-ADLISYHPPIFRPKKRTTWTNWKRLVIRALENVGITYSPHTAADAPQGVNNMLAK 116
   -||| : : : : : ||| : : : : : ||||| ||| ||||| : : :
Db 63 KLVSSIVAYHPPIFRGKATIMEDPOKSLKLAEGIHVYSPHTAADAVDQVNDMLAQ 122

QY 117 GLGACTSRPIHPSKAPVYPTGEGNHRVFNVTYDLDKVASAVGIDGVSPTSARTGN 176
   | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 GING-----GRRNKK-SVYPTQ----- 138

QY 177 EQQTRINLCTOKALQVDFLSRNKKQLYOKTEILLSLEKPLLHTGNGRLCTIDESVSLA 236
   | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 139 -----QNSVNAEAE-----GVRICELKIPPTLR 162

QY 237 TMDIRIKRLKLSHIRALVGRILSEGVVVAICAGSSGVLOGVADLYLIGEMSHHD 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 163 ELVQRAKELTGLQVVOACAPNG--LDSHISKVSLCAGSGSVVNMNDADLYFGELSHQ 220

QY 297 TLDAASGIVVILCEHSNTERGFSLDL--BDMLDS-HLEN-KIITLSTDRPL 347
   | : : : : : ||||| : : : : : | : : : : : | : : : : :
Db 221 VLAAMAKGISVILCGHSNTERGTLKDYKCKLASSFKEGVDAVNIYSSMDADPL 275

RESULT 2
S64243
```

hypothetical protein YGL221c - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein G1020
C:Species: *Saccharomyces cerevisiae*
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
C:Accession: S64243
R:Reger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64071
A:Accession: S64243
A:Molecule type: DNA
A:Residues: 1-288 <R1E>
A:Cross-references: EMBL:Z72743; NID:g1322868; PIDN:CAA96937.1; PID:g1322869; MIPS:YGL222
C:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:NIF3
A:Cross-references: SGD:S0003189; MIPS:YGL221c
A:Map position: 7L
C:Superfamily: conserved hypothetical protein YGL144c

Query Match 21.4%; Score 384.5; DB 2; Length 288;
Best Local Similarity 28.6%; Pred. No. 2,1e-23;
Matches 104; Conservative 59; Mismatches 99; Indels 103; Gaps 11;

3 LKALLSLNDFASLSFAE-SMDNVGLLVESPPTHTVNT-----LFTLNDITFEEMEEV 54
10 LDKLVRSITKFFYPQKAYADKSMDNTGLIDCSAQTADANAKTKVLLVLDLTKSYAOEA 69
55 LQKKADLLISYHPPIFPMPKRIPTWNT-WKERLVIRALENRYGVSPTHAYDAPOGVNNM 113
70 VQANCAVIAVAHFFIPFSMNRLSPHTNPQHTAFLKIDYGISVYCPHRAVDAARGVNDM 129
114 LAKGLIAGCTSRPIHPSKAPNYPTGEGNHRVEENVYTDLDKVMASVKGIDGVSVT-SFSA 172
130 LVKGLN-----NGENVAKSAYAL 146
173 RFGNEQGTIRINLNCTQKALMQVDFLSRNKQLDYKTELLSLKPLLLHTGMERLCTLDES 232
147 ETVSGE-----TDLL-----IGGFEVEFNKD 168
233 VSLATMDIRIKRHLKSHIRLALGVGRILSESQKV--VALCAGSSSVLYQGV--EADLYL 288
169 ISLEIVKNNKRVLRVPYVQVASLAPSAVMQKIKKVAVCAVGSSGSGVFKQLEKEDVLYX 228
283 TGESSHHDITLDAASQGINVLYCEHSNTERGLSLDRDL--DSHLKKNINILSTDRD 345
229 TGESSHHEVLYKWEKMGKTVIVCNHNSNTERGLDVMKGLDDEGH---EVAVSKMDCD 283
346 PLQV 349
111
284 PLTV 287

RESULT 3
A69954
conserved hypothetical protein yqfO - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C:Accession: A69954
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertier
C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chai
A.; Ehrlich, S.D.; Emmertson, P.T.; Entian, K.D.; Erlingsson, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Poulsen, D.; Fritzt, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gallen
lech, J.; Hartwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsfeld, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
V. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolet, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schreuter, R.; Scoffone, F.; Sekiguchi, J.; Sekowski, A.; Serorom
A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zunnun, E.; Yoshikawa, H.; Dauchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A:Reference number: A699580; MUID:98044033; PMID:9384377
A:Accession: A69954
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-373 <KUN>
A:Cross-references: GB:A699116; GB:AL009126; NID:g2634723; PIDN:CABJ4447.1; PID:g26349
A:Experimental source: strain 168
C:Genetics:
A:Gene: ynfO

Query Match 15.9%; Score 285.5; DB 2; Length 373;
Best Local Similarity 26.1%; Pred. No. 3e-15;
Matches 99; Conservative 79; Mismatches 143; Indels 59; Gaps 17;

OY 6 LLSSINLFASISFAESMDNVGL-----LVPSPPHTVNTFLFNDLFEVEAEVYLQKKADL 61
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 10 IQLFEQFSKRAYVEGDKIGLGITLNKP-----IKNWATLDLVLESVIDEAIKEKVLD 64
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 62 ILSYHPDIFRPMKRITWNWKERLIVALENRVGISPHPTAYDAPOGVNMMLAKGIAC 121
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 65 IIAHHPIPLSLKHISPDOPAGRLIEKLKHDIYAHAHNLVDADGDVNDLLAEALELS 124
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 122 TSPRIHSKAPN-----PTE-----GN-----HRYEENVATYDDLOLVMS 157
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 125 ETEVL----APTGYDPLKLAVVPKYEEOVRALALDNAGAHIGEY--SHCAFSESGTG 178
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 158 AVKGIDGVSVYSFSAFTGNEE---QTFININCTOKALMOYVDFLSRNKOLOYKT--ELIS 212
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 179 SFRKLDQAK--PFIGEVGELEIYVEHYLEVFPEKVSFKAVIANIMAKISHP-YEEVAVDIYP 235
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 213 LEKFLILHTMGRLCTIDESVSLATMIDRIKRLHKESHIRLAGVGTLESSQVVVALCA 272
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 236 VEQ--TPAEKGGVGRVGLTKNEMTLKFALFFVKDKLDVANGVHR--V-G-DASMAKKAVALG 290
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 273 GSGGSVLOGVE---ADLYLTGEMSHHDLPDAOSGINVIICESHSTFERGFLSDLRMLDS 329
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 291 GDGKKYIHNAKKRKADYYVTGDLTFHYHADMMGLAVNDPGH-YAEKIKEGVTRKLTSS 349
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 330 HLENK---INIISETDRDP 346
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 350 MCNDKRFGVNIWFSETDTPN 369
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 4
F89936
Conserved hypothetical protein SA1388 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: F89936
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-H, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C., Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89936
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-366 <KUR>
A:Cross-references: GB:BA000018; PID:g13701357; PIDN:BABA2651.1; GSFD:BN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1388

Query Match 15.5%; Score 278; DB 2; Length 366;
Best Local Similarity 26.0%; Pred. No. 1.2e-14;
Matches 105; Conservative 67; Mismatches 140; Indels 92; Gaps 18;

OY 1 MDKALLSLSDPFASLSFAESMDNVGLVPSPPHTVNTFLFNDLFEVEAEVYLQKKAD 60
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1 MKADIWMTLDHNHFVPSFAESMDNVGLIGDGVEYTVGL-TALDCILEVYNNAIERGYN 59
 | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 61 LILSYHPDIFRPMKRITWNWKERLIVRAL-ENRVGISPHPTAYDAAPGVNMMLAKGLG 119

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Db      60 TTIISHHPLFEKGVTSKANGY--GLITIRKLIQHDIMLHMTMDVNPYGVNMLAKAMG 117
OY      120 ACSRRIPHSKAPNPT-----EGNHRVEF-----144
Db      118 LKNISITINNOQVYVYVQYIIPDNVGPFKDLSENGLAOGEYECFEFSEGRGPKPV 177
OY      145 -NWNVT-ODLDKVMASVKGIDGVSYSFSARTGNEBQTRINLCTOKALMQVVDPLSRNK 202
Db      178 GEMNPTIGQIDK-----IEDVDEKI-----ERMIDAYOK-----SRAE 211
OY      203 QLYOK-----TEILSEKPLLLHTGGRICLTDESVSLATMIDRIKRLKLSHRLA 254
Db      212 QLTQKHYPETPFDEFIEIKQTSLY--GLGVMALEVNONMTLEDFPADIKSLINIPSVRF- 268
OY      255 LCGVRLLESQVKNVVALCAGS-----SSVAGVEADLYLTGESHHDITDAAQGINVL 309
Db      269 --VGES--NOKIKALITGSGIGEYQAVQOG--ADVFTYGDIKHHDALDAKIHGNVLD 323
OY      310 CEHSNTERGFLSDRLDMSHLE-NKINIL--SETDRDPLQVY 350
Db      324 INH-YSEYWKESGLKTLNMWFIKINIDVEASTINTDFOYI 366

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RESULT 5

uncharacterized protein of YbgI/Acr family [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: G97060
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: G97060
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-268 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK9274.1; PID:g15024233; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1303

Query Match 14.7%; Score 264; DB 2; Length 268;
 Best Local Similarity 21.3%; Pred. No. 9.8e-14;
 Matches 75; Conservative 63; Mismatches 118; Indels 96; Gaps 6;

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OY      1 MDKALLSLINDFASLSFAESMDNVGLVPEPPHTVNTLFLTNDLTEEYMEEVLOKKAD 60
Db      3 LKWKDCNIIEDEPAPISLKEDFDNGLMVGDRFA-SVDAIMTALDCTMDVIDAIEKNCN 61
OY      61 LLIISYPIFRPKKRTITMTWKERLYIRALENVGSIYSPHTAYDAAPQVNNMLAGLGA 120
Db      62 MITTHPIIFKRSKTIPTDLTKKIKIISNNININYSATTNDSYKGDINDAVNVLIG- 120
OY      121 CTSRPIHPSKAPNPTPEGNHRVEFNVTQDDLDKVMASVKGIDGVSYSFSARTGNEQRT 180
Db      121 -----120
OY      181 RINLCTOKALMQVVDPLSRNKQLYOKTEILSEKPLLLHTGGRICLTDESVSLATMID 240
Db      121 -----FDKSSILAKNNNAVKRAGIGRAVELEQNMTLKELCD 156
OY      241 RIKRHLKSHIRALGVGRLESQVNVVALCAGSGSSVLAGVE---ADLYLTGESHHDIT 297
Db      157 RYVESRKIQLSRKCGDEDKIHS---FAVINGSGODFEFEARKRGDCLITDGTSYHYV 212
OY      298 LDAASGIVNITLCEHSNTERGFLSDRLDMSHLENK-IR--IILSETDRP 346
Db      213 SDINEMNINAVIDAGHGTETPMSVYVMSKLEGALHKMGKINTPIIVSONNIDP 264

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RESULT 6
 Db3822
 hypothetical protein BH1380 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: D83822
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D83822
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-372 <STNO>
 A:Cross-references: GB:AP001511; GB:BA000004; MID:g10173727; PIDN:BA05099.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH1380

Query Match 14.6%; Score 263.5; DB 2; Length 372;
 Best Local Similarity 24.9%; Pred. No. 1.8e-13;
 Matches 89; Conservative 80; Mismatches 141; Indels 47; Gaps 12;

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OY      25 VGLVPEPPHTVNTLFLTNDLTEEYMEEVLOKKADLIISYHPPIFRPKRTITMTWKER 84
Db      32 IGTINKP-----IORVLTALDVMEVSIDEAIEFGAELILAHNPPIFRPLSSIRTPRAYGR 86
OY      85 LVIRALENRGITSPTHTAYDAAPQVNNMLAKGLGACTSPRIHPSKAPNPTGNNRVER 144
Db      87 IIRKAKIHDITLYIAAHNLDITRGVNDMAADLAKGIDIVLAP-----TTSSLVKLVV 141
OY      145 NVNVTQDDLDKVMASVKGIDGVSYSFSARTGNEQRT-----RINLCTOKALMQVVD 197
Db      142 FVPHTH-TDQVREALGRAGGCHGNISYCTFNKSGTGFPEKCTNPFICQGALEVEE 200
OY      198 L-----SRNKQLYOKTEILSEKPLL-LH-----TGMRICLTDESVSLATMI 239
Db      201 LKTIETITEGQKKVAAAMIKSHPEEPADVPLPLANEGETLGLGRIGVLEHSMTLDEFA 260
OY      240 DRIKRLKLSHIRALGVGRLESQVKNVVALCAGSGSSVLAGV---EADLYLTGESHHD 296
Db      261 KQVKAFFDVPYARV---VG-SLETOIRKVAIVLGGDKRYMAHALRKGAADVIVGDDVYHYV 316
OY      297 TLDAASGIVNITLCEHSNTERGFLSDRLDMSHLENK--INILSETDRDPLQVY 350
Db      317 PHDALMDGLNITVPGH-NVEKIMQGVKELEKLDKKKIDTEVAVSSVTFDPTFI 372

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RESULT 7

conserved hypothetical protein lln1489 [imported] - Listeria innocua (strain C11p1126
 C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AH1618
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussaugel, O.; Entlian, K.D.; Feiht,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1618
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-373 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAC096720.1; PID:g16413962; GSPDB:GN00178
 A:Experimental source: strain C11p1126
 C:Genetics:
 A:Gene: lln1489

Query Match 14.2%; Score 256; DB 2; Length 373;
 Best Local Similarity 22.5%; Pred. No. 7.1e-13;

[illegible]

RESULT 8
AD1256
conserved hypothetical protein Imo1452 [Imported] - *Listeria monocytogenes* (strain EGD-
C) Species: *Listeria monocytogenes*
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
R.Glaeser, P. Frangouli, L. Buchrieser, C. Amend, A. Baquero, F. Berche, P. Bloeker
D., Dominguez-Bernal, G. Duclaud, E. Durand, L. Dussurget, O. Entlian, K.D. Fsihl, H.
D., Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Knapkat, G.; Madueno, E.; Maitournam, A.; Ma
ör, C.; Schleuter, T.; Simoes, N.; Tierrier, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ
A.Title: Comparative genomics of *Listeria* species.
A.Reference number: AB1077; MUID:21537279; PMID:11679669
A.Accession: AD1256
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-373 <GUI>
A.Cross-references: GB:NC_003210; PIDN:CAC99530.1; PID:q16410881; GSPDB:GN00177
A.Experimental source: strain EGD-e
C.Genetics:
A.Gene: Imo1452

[illegible][illegible]

RESULT 9
DB1341
hypothetical protein Cj0705 [imported] - Campylobacter jejuni (strain NCTC 1168)
C.Species: Campylobacter jejuni
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C.Accession: DB1341
R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, T.; Davis, A.A.; Dougan, G.; Fraser, H.; Harris, D.S.; Holt, K.E.; Jones, S.J.; Karpman, P.; Martin, J.F.; Morgan, R.D.; Parkhill, J.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyilet, A.; Whitehead, S.; Barratt, C.E.; Brown, L.M.; Carver, T.F.; Clark, F.; Clifton, E.; Collins, M.; Coulthurst, C.; Davies, J.; De Jong, A.; Denby, L.; Dingle, J.; Donachie, A.; Edwards, J.; Evans, J.; Frost, A.; Fulton, R.; Garner, S.; Gilbert, J.; Gordon, S.; Haywood, V.E.; Heffernan, P.; Hendry, A.P.; Higgs, K.G.; Hughes, K.; Hunt, A.; James, K.D.; Johnston, I.R.; Keane, T.; Kell, M.B.; Kenton, F.M.; Kirkness, E.; Kumar, A.; Laing, J.; Leach, M.C.; Little, D.; MacArthur, C.T.; MacLennan, S.; McAnulty, S.; McEldowney, S.; McIninch, J.; McQuinn, K.; Mellor, J.; Miller, J.; Mitchell, J.; Mountford, S.; Murray, K.; Nelson, A.; O'Connell, B.; O'Donnell, C.; O'Leary, E.; Paterson, G.; Pearson, T.A.; Perkins, J.; Petts, C.; Plowright, R.; Quinn, C.; Rawlings, S.; Roddam, D.; Ross, M.; Saunders, D.; Seakins, J.; Sharp, J.; Skusek, D.; Smith, R.; Sprague, A.; Staden, R.; Struelens, L.; Taggart, J.; Taylor, K.; Teague, P.; Thomson, N.; Todd, J.; Tooke, D.; Unwin, P.; Van Dongen, P.; Venter, A.; Walker, A.; Ward, M.; Waters, K.; Whittam, T.S.; Whittam, T.S.; Woodward, G.; Wright, A.; Young, I.P.; Zhang, Y.
A.Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A.Reference number: AB1250; MUID:20150912; PMID:10688204
A.Accession: DB1341
A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-241 <PAR>
A.Cross-references: GB:AL139076; GB:AL111168; NID:65968128; PIDN:CAB72979..1; PID:65966
A.Experimental source: serotype O2, strain NCTC 1168
C.Genetics:
A.Gene: Cj0705

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Query Match          12.5%  Score 225;  DB 2:  Length 241;
Best Local Similarity 19.2%  Fred. No. 1.2e-10;
Matches 68;  Conservative 63;  Mismatches 95;  Indels 128;  Gaps 9;

OY      1 MDLKALLSLINDEFASLSFAESMDNNGLLVEESPPIHTVTLFLTNDLTDEEVEEVLQAKAD 60
      1 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB      1 KMLSTIYNFLDQLSFNIQESWDNNGILLGRDSE-ISTVYLSIDIDENITKEASEN--S 57
      1 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

OY      61 LILSHPIPIFRPMKRITVNTWKERLVITALENRGITYSPHATYDAAPGVANNMLAKIGGA 120
      61 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB      58 LIITHHPPLIFKQIKNDLYDKTYPRAFIKEMIKKNISLISMHTNYDS----- 103
      58 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

OY      121 CTSRPIHPSKAPNYPTEGHNHRYEFNVNVTODLDKMASAVKIDGVSYSFGARTGNEBOT 180
      121 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB      104 -----HLNFTYTEE-----ILGFR----- 117
      104 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

OY      181 RINLNCOTAKALQVVDPLSRNKQLYKTEIISLEKPELLHMGRLCTLDESVSLATMID 240
      181 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB      118 -----ISFKKFLIY-----VENSMSFEALCD 139
      118 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

OY      241 RIKRHLKSHITLALGVGTLESOYKVALAGSGSSVLQGVYADLYLTGESHHDPTLDA 300
      241 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB      140 WKKKRLNIQLR-----VSDCGKKDKIRKALTCGSGDLISKVDACFISGDFKHYQALEA 195
      140 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

OY      301 ASQGIIVNICEHSNTERGF---LSDLRMLDLSHLENKRNIIISLSTDRDPLQVW 350
      301 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB      196 LSNQISLIDLGHFESRFTSQCLANDKNL-----PLQVI 230
      196 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 10
B70777
hypothetical protein RV2230c - Mycobacterium tuberculosis (strain H37RV)
C:/Species: Mycobacterium tuberculosis
C:/date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:/Accession: B70777
R:/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
/ Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

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